

Amendments

The specification is amended to update the cross-reference, and correct a typographical error in a sequence reference number; the claims are amended to require hybridization under stringent conditions, and to recite that the hybridization is between nucleic acids; new claims 21-26 recite an exemplified stringent condition (specification, p.7, lines 10-15); and new claims 27-32 require that the polynucleotide comprise the recited SEQ ID NO.

35USC112, second paragraph.

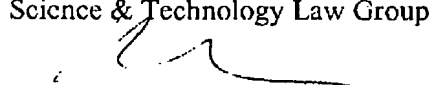
Afc1 and Rce1 are definite terms in the art for specific CAAX proteases. The Action cites "Face-2"; however the term "Face-2" is just a known synonym for RCE1 – they are the same thing. See, UniProtKB/Swiss-Prot entry Q9Y256 for Face-2 (attached).

35USC112, first paragraph

The recited genus is circumscribed by both structure (hybridizing under stringent conditions to, or comprising a recited sequence) and function (encoding a CAAX protease that mediates the proteolytic removal of an AAX tripeptide from a prenylated CAAX protein). New claims 21-26 specifically define required hybridization and wash conditions; and new claims 27-32 specifically require that the polynucleotide comprise the recited SEQ ID NO.

The Examiner is invited to call the undersigned with any suggestions for amending the claims or further clarifying any of the foregoing. Please charge any required fees, including extension fees, or credit any overcharges for this communication to our Dep. Acct. No.19-0750 (order B96-021-6).

Respectfully submitted,
Science & Technology Law Group



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Enc. UniProtKB/Swiss-Prot entry Q9Y256 for Face-2 (3p.)

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UniProtKB/Swiss-Prot entry Q9Y256



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[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	FACE2_HUMAN
Primary accession number	Q9Y256
Secondary accession numbers	None
Integrated into Swiss-Prot on	April 27, 2001
Sequence was last modified on	November 1, 1999 (Sequence version 1)
Annotations were last modified on	September 19, 2006 (Entry version 40)

Name and origin of the protein

Protein name	CAAX prenyl protease 2
Synonyms	EC 3.4.22.- Prenyl protein-specific endoprotease 2 Farnesylated proteins-converting enzyme 2 FACE-2 hRCE1
Gene name	Name: RCE1 Synonyms: FACE2, RCE1A
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

References

[1] NUCLEOTIDE SEQUENCE [MRNA].

TISSUE=Ovary;

DOI=10.1006/geno.1999.5834; PubMed=10373325 [NCBI, ExPASy, EBI, Israel, Japan]

Freije J.M.P., Blay P., Pendas A.M., Cadinanos J., Crespo P., Lopez-Otin C.;

"Identification and chromosomal location of two human genes encoding enzymes potentially involved in proteolytic maturation of farnesylated proteins.";

Genomics 58:270-280(1999).

[2] NUCLEOTIDE SEQUENCE [MRNA], AND CHARACTERIZATION.

DOI=10.1074/jbc.274.13.8379; PubMed=10085068 [NCBI, ExPASy, EBI, Israel, Japan]

Otto J.C., Kim E., Young S.G., Casey P.J.;

"Cloning and characterization of a mammalian prenyl protein-specific protease.";

J. Biol. Chem. 274:8379-8382(1999).

[3] CHARACTERIZATION.

DOI=10.1006/abio.2000.4795; PubMed=11038283 [NCBI, ExPASy, EBI, Israel, Japan]

Hollander I., Frommer E., Mallon R.;

"Human ras-converting enzyme (hRCE1) endoproteolytic activity on K-ras-derived peptides.";

Anal. Biochem. 286:129-137(2000).

Comments

- **FUNCTION:** Proteolytically removes the C-terminal three residues of farnesylated and geranylated proteins. Seems to be able to process K-Ras, N-Ras, H-Ras, RAP1B and G-gamma-1.
- **SUBCELLULAR LOCATION:** Endoplasmic reticulum; endoplasmic reticulum membrane; multi-pass membrane protein (*By similarity*).
- **TISSUE SPECIFICITY:** Ubiquitous.
- **SIMILARITY:** Belongs to the peptidase U48 family [view classification].

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Cross-references**Sequence databases**

EMBL Y13835; CAB46278.1; -; mRNA. [EMBL / GenBank / DDBJ] [CoDingSequence]
AF121951; AAD22632.1; -; mRNA.[EMBL / GenBank / DDBJ] [CoDingSequence]

UniGene Hs.591964

3D structure databases

ModBase Q9Y256.

Protein-protein interaction databases

DIP Q9Y256.

Protein family/group databases

MEROPS U48.002; -.

2D gel databases

SWISS-2DPAGE Get region on 2D PAGE.

Organism-specific gene databases

HGNC HGNC:13721; RCE1.

GeneCards RCE1.

GeneLynx RCE1; Homo sapiens.

GenAtlas RCE1.

MIM 605385; gene. [NCBI / EBI]

HOVERGEN [Family / Alignment / Tree]

Gene expression databases

CleanEx HGNC:13721; RCE1.

ArrayExpress Q9Y256; -.

Ontologies

GO GO:0005887; Cellular component: integral to plasma membrane (*traceable author statement*).
GO GO:0008487; Molecular function: prenyl-dependent CAAX protease activity (*traceable author statement*).
GO GO:0006508; Biological process: proteolysis (*traceable author statement*).
QuickGo view.

Family and domain databases

IPR003675; Abi.

InterPro Graphical view of domain structure.
 Pfam PF02517; Abi; 1.
 Pfam graphical view of domain structure.
 ProDom [Domain structure / List of seq. sharing at least 1 domain]
 BLOCKS Q9Y256.

Genome annotation databases

Ensembl ENSG00000173653; Homo sapiens. [Contig view]
 KEGG hsa:9986; -.

Other

SOURCE RCE1; Homo sapiens.
 ProtoNet Q9Y256.
 UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Endoplasmic reticulum; Hydrolase; Membrane; Transmembrane.

Features



Feature table viewer



Feature aligner

Key	From	To	Length	Description	PTID
CHAIN	1	329	329	CAAX prenyl protease 2.	PRO_0000194830
TRANSMEM	25	45	21	Potential.	
TRANSMEM	75	95	21	Potential.	
TRANSMEM	112	132	21	Potential.	
TRANSMEM	186	206	21	Potential.	
TRANSMEM	229	249	21	Potential.	
TRANSMEM	254	274	21	Potential.	
TRANSMEM	283	303	21	Potential.	

Sequence information

Length: **329 AA** [This is the length of the unprocessed precursor]

Molecular weight: **35833 Da** [This is the MW of the unprocessed precursor]

CRC64: **BA8F764651172BFA** [This a checksum on the sequence]

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      10      20      30      40      50      60
MAALGGDGLR LLSVSRPERP PESAALGGLG PGLCCWVSVF SCLSLACSYV GSLYVWKSEL

      70      80      90     100     110     120
PRDHPAVIKR RFTSVLVVSS LSPLCVLLWR ELTGIQPGTS LLTLMGFRLE GIFPAALLPL

     130     140     150     160     170     180
LLTMILFLGP LMQLSMDCPC DLADGLKVVL APRSWARCLT DMRWLRNQVI APLTEELVFR

     190     200     210     220     230     240
ACMLPMLAPC MGLGPAVFTC PLFFGVAHFH HIIEQLRFRQ SSVGNIFLSA AFQFSYTAVF

     250     260     270     280     290     300
GAYTAFLFIR TGHLLGPVLC HSFCNYMGFP AVCAALEHPQ RRPLLAGYAL GVGLFLLLLQ

     310     320
PLTDPKLYGS LPLCVLLERA GDSEAPLCS
  
```

Q9Y256 in
FASTA format